

GGAGGGCAGCAAGGACGGCACCAAGGGAGCTACCCCATGGACAGGGCCCCACAGAGACACCACCGGACAT
 CTCGGGAGCTGCTGGCTGCAAAGAAGACCCACACCTCACAAATTGAAGTGATCCCTTGCAAGATCTGTGG
 GGACAAGTCATCTGGGATCCACTACGGGGTTATCACCTGTGAGGGGTGCAAGGGCTTCTTCCGCCGCAGC
 CAGCAGTGTAATGTGGCCTACTCCTGCACGCGTCAGCAGAACTGCCCCATTGACCGAACCAGCCGCAACC
 GATGCCAGCATTGCCGCCTGCAGAAGTGCCTGGCTCTGGGCATGTCCCGAGATGCTGTCAAGTTTGGCCG
 AATGTCCAAGAAGCAGAGGGACAGTCTACATGCAGAAGTGCAGAAACAACCTGCAACAGCAGCAGCAACAG
 GAACAAGTGGCCAAGACTCCTCCAGCTGGGAGCCGCGGAGCAGACACACTTACATACACTTTAGGGCTCT
 CAGATGGGCAGCTACCACTGGGCGCCTCACCTGACCTACCCGAGGCCTCTGCTTGTCCCCCTGGCCTCCT
 GAGAGCCTCAGGCTCTGGCCCCACCATATTCCAATACCTTGGCCAAAACAGAGGTCCAGGGGGCCTCCTGC
 CACCTTGAGTATAGTCCAGAACGAGGCAAAGCTGAAGGCAGAGACAGCATCTATAGCACTGACGGCCAAC
 TTACTCTTGGAAGATGTGGACTTCGTTTTGAGGAAAACCAGGCATCCTGAACTTGGGGAACCAGAACAGGG
 TCCAGACAGCCACTGCATTCCCAGTTTCTGCAGTGCCCCAGAGGTACCATATGCCTCTCTGACAGACATA
 GAGTACCTGGTACAGAATGTCTGCAAGTCCTTCCGAGAGACATGCCAGCTGCGACTGGAGGACCTTCTAC
 GGCAGCGCACCAACCTCTTTTACGGGAGGAGGTGACCAGCTACCAGAGGAAGTCAATGTGGGAGATGTG
 GGAGCGCTGTGCCACCACCTCACTGAGGCCATTCACTATGTGGTGGAGTTTGCCAAGCGGCTTTAGGC
 TTCATGGAGCTCTGCCAGAATGACCAGATCATACTACTGACAGCAGGAGCAATGGAAGTCGTCCTAGTCA
 GAATGTGCAGGGCCTACAATGCCAACAACCACACAGTCTTTTTTGAAGGCAAATACGGTGGTGTGGAGCT
 GTTTTCGAGCCTTGGGCTGCAGCGAGCTCATCAGCTCCATATTTGACTTTTCCCACTTCTCAGCGCCCTG
 TGTTTTTCTGAGGATGAGATTGCCCTCTACACGGCCCTGGTTCTCATCAATGCCAACCCTCCTGGGCTCC
 AAGAGAAGAGGAGAGTGAACATCTGCAATACAATTTGGAAGTGGCTTTCCATCATCATCTCTGCAAGAC
 TCATCGACAAGGCCTCCTAGCCAAGCTGCCACCCAAAGGAAAACCTCCGGAGCCTGTGCAGCCAACATGTG
 GAAAAGCTGCAGATCTTCCAGCACCTCCACCCCATCGTGGTCCAAGCCGCTTCCCNCCACTCTATAAGG
 AACTCTTCAGCACTGATGTTGAATCCCTGAGGGGCTGTCAAAGTGATCTGGAGGAAGGACAACCTTTCTA
 TTTCTTCAGCCCTCTGACCCGCTCTCCCTGGACTCCCTTCACCCAGCCTTTCCCTTTCTGCACTCTATGA
 AGGGTGGTATCCCTAGGAGTAAGCAAATCCTAAGACTGATTTTCTGCCCCTAGGCTTGCCTTGTAGGACA
 ACAGCAGCAAGTGATGGAGAAAAGGCTTGTTATGTTTGATTTCCCATAGTTCCACCCTGGCTTCTGGAA
 GCTGTGGGGTAGATGGGATAGAGATAGGATGACCAAGTCAAATAAAAAACAGACTGACAATCAGCAGGGA
 TAAATCCAGGTACCTGGGATAAGGAGAACTCAAATCTAGGCTTGAAAGCTAATAACAGTCCTTTCAATAC
 CTCATTGTATTTCCCATGGGTCTCCTGGGGGACATGGATCTAGCTCAGAGACTGGTGGCAAGCCCCC
 AGAAGGACCTGTATATAATAAGAATATAGATTCCCTG (SEQ ID NO:1)

MDRAPQRHRTSRELLAAKKTHTSQIEVIPCKICGDKSSGIHYGVITCEGCKGFFRRSQQC
 VAYSCTRQNCPIDRTSRNRCQHRLQKCLALGMSRDAVKFGRMSKKQRDSLHAEVQKQ
 LQQQQQQEQVAKTPPAGSRGADTLTYTLGLSDGQLPLGASPDLPASACPPGLLRASGSGPP
 YSNTLAKTEVQGASCHLEYSRPERGKAEGRDSIYSTDGQLTLGRCLRFEETRHPPELGEPEQG
 PDSHCIPSFCSAPEVPYASLTDIEYLVQNVCKSFRETQQLRLEDLLRQRTNLSREEVTSYQR
 KSMWEMWERCAHHLTEAIQYVVEFAKRLSGFMELCQNDQIILLTAGAMEVVLVRMCRA
 NANNHTVFFEGKYGGVELFRALGCSELISIFDFSHFLSALCFSEDEIALYALVLINANRPL
 QEKRRVEHLQYNLELAFHHHLCKTHRQGLLAKLPKGLRSLCSQHVEKLQIFQHLHPIV
 QAAFPLYKELFSTDVESPEGLSK (SEQ ID NO:2)

FIGURE 1

2025-07-07 10:55:50

underlined = deleted in targeting construct

[] = sequence flanking Neo insert in targeting construct

GGAGGGCAGCAAGGACGGCACCAAGGGAGCTACCCCATGGACAGGGCCCCACAGAGACAC
 CACCGGACATCTCGGGAGCTGCTGGCTGCAAAGAAGACCCACACCTCACAAATTGAAGTG
 ATCCCTTGCAAGATCTGTGGGACAAGTCATCTGGGATCCACTACGGGGTTATCACCTGT
 GAGGGGTGCAAG [GGCTTCTTCCGCCGAGCCAGCAGTGTAATGTGGCCTACTCCTGCACG
 CGTCAGCAGAA] CTGCCCCATTGACCGAACCAGCCGCAACCGATGCCAGCATTGCCGCCTG
CAGAAGTGCCTGGCTCTGGGCATGTCCCGAGATGCTGTCAAGTTTGGCCGAATGTCCAAG
AAGCAGAGGGACAGTCTACATGCAGAAGTGCAGAAACAACCTGCAACAGCAGCAGCAACAG
GAACAAGTGGCCAAGACTCCTCCAGCTGGGAGCCGCGGAGCAGACACACTTA [CATACT
 TTAGGGCTCTCAGATGGGCAGCTACCACTGGGCGCCTCACCTGACCTACCCGAGGCCTCT
 GCTTGTCCCCCTGGCCTCCTGAGAGCCTCAGGCTCTGGCCCACCATATTCCAATACCTTG
 GCCAAAACAGAGGTCCAGGGGGCCTCCTGCCACCTTGAGTATAGTCCAGAACGAGGCAAA
 GCTGAAGGCAGAGACAGCATCTATAGCACTGACGGCCAACCTTACTCTTGGAAGATGTGGA
 CTTTCGTTTTGAGGAAACCAGGCATCCTGAACTTGGGGAACCAGAACAGGGTCCAGACAGC
 CACTGCATTCCCAGTTTTCTGCAGTGCCCCAGAGGTACCATATGCCCTCTCTGACAGACATA
 G] AGTACCTGGTACAGAATGTCTGCAAGTCCTTCCGAGAGACATGCCAGCTGCGACTGGAG
 GACCTTCTACGGCAGCGCACCAACCTCTTTTACGGGAGGAGGTGACCAGCTACCAGAGG
 AAGTCAATGTGGGAGATGTGGGAGCGCTGTGCCACCACCTCACTGAGGCCATTCACTAT
 GTGGTGGAGTTTGCCAAGCGGCTTTCAGGCTTCATGGAGCTCTGCCAGAATGACCAGATC
 ATACTACTGACAGCAGGAGCAATGGAAGTCGTCCTAGTCAGAATGTGCAGGGCCTACAAT
 GCCAACAACCACACAGTCTTTTTTTGAAGGCAAATACGGTGGTGTGGAGCTGTTTCGAGCC
 TTGGGCTGCAGCGAGCTCATCAGCTCCATATTTGACTTTTCCCACTTCTCAGCGCCCTG
 TGTTTTTCTGAGGATGAGATTGCCCTCTACACGGCCCTGGTTCTCATCAATGCCAACCGT
 CCTGGGCTCCAAGAGAAGAGGAGAGTGGAACATCTGCAATACAATTTGGAAGTGGCTTTC
 CATCATCATCTCTGCAAGACTCATCGACAAGGCCTCCTAGCCAAGCTGCCACCCAAAGGA
 AAATCCGGAGCCTGTGCAGCCAACATGTGGAAAAGCTGCAGATCTTCCAGCACCTCCAC
 CCCATCGTGGTCCAAGCCGCCTTCCCNCCACTCTATAAGGAACTCTTCAGCACTGATGTT
 GAATCCCCTGAGGGGCTGTCAAAGTGATCTGGAGGAAGGACAACTTTCTATTTCTTTCAG
 CCTCTGACCCGTCTCCCTGGACTCCCTTCACCCAGCCTTTCCCTTTCTGCACTCTATGA
 AGGGTGGTATCCCTAGGAGTAAGCAAATCCTAAGACTGATTTTCTGCCCTAGGCTTGCC
 TTGTAGGACAACAGCAGCAAGTGATGGAGAAAAGGCTTGTTATGTTTGATTCCCATAAG
 TTCCACCCTGGCTTCTGGAAGCTGTGGGGTAGATGGGATAGAGATAGGATGACCAAGTCA
 AATAAAAAACAGACTGACAATCAGCAGGGATAAATCCAGGTACCTGGGATAAGGAGAAGT
 CAAATCTAGGCTTGAAAGCTAATAACAGTCCTTTCAATACCTCATTTGTATTTCCCATGG
 GTCCTCCTGGGGGACATGGATCTAGCTCAGAGACTGGTGGCAAGCCCCCAGAAGGACCT
 GTATATAATAAGAATATAGATTCTG (SEQ ID NO:1)

FIGURE 2A

Gene Sequence
Structure *

252 bp

Sequence Deleted

472 bp

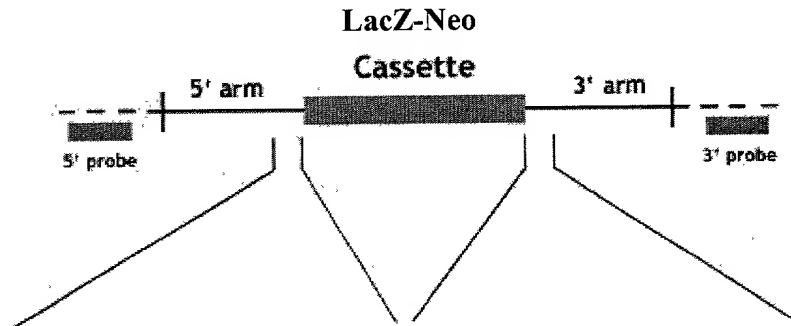
Size of full-length
cDNA: 2066 bpTargeting Vector*
(genomic sequence)

Construct Number: 651

Arm Length:

5': 1.6 kb

3': 2.5 kb



5'>CAGGGTCCATCACAATTATAC
AGTGGAGGTTTCGGGGACTTTGGTG
GATGTAGAAATTCTTGAGACCAGT
GCACATGAATTGGAGGTCCCTGGG
ACCACCTCAAACCTCCGAGAGGGTG
GGATAAGCAGTTTCTGTTTCCCAG
GGCTTCTTCCGCCGAGCCAGCAG
TGTAATGTGGCCTACTCCTGCACG
CGTCAGCAGAA<3'
(SEQ ID NO:3)

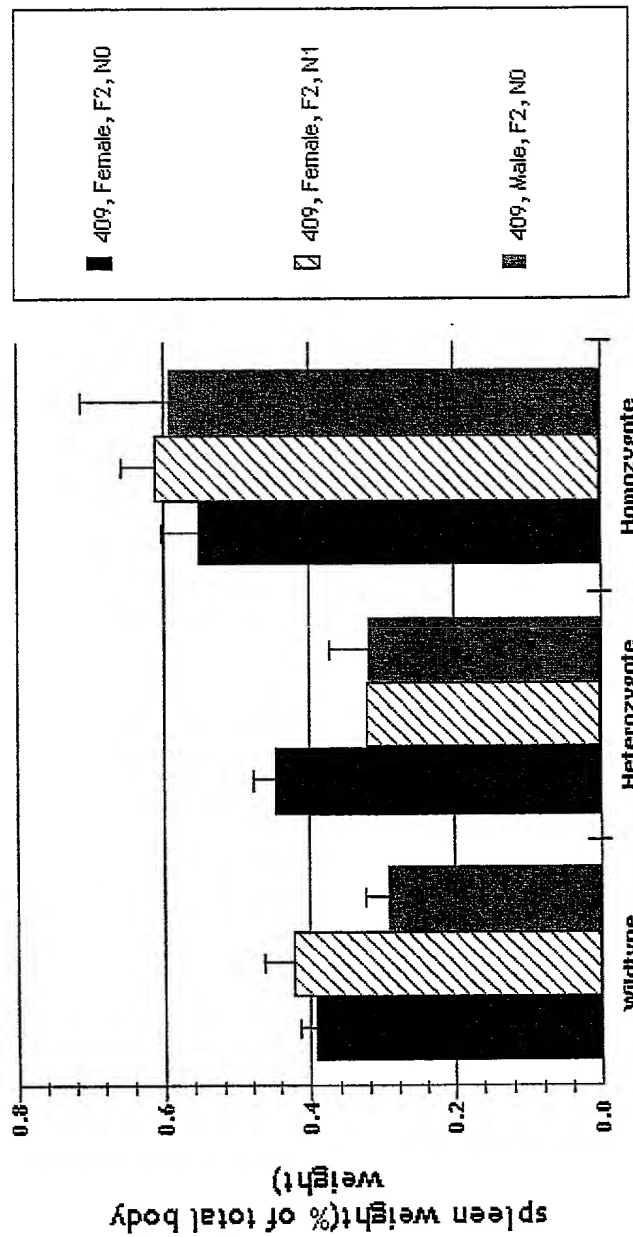
5'>CATACACTTTAGGGCTCTCAG
ATGGGCAGCTACCACTGGGCGCCT
CACCTGACCTACCCGAGGCCTCTG
CTTGTCCTCCCTGGCCTCCTGAGAG
CCTCAGGCTCTGGCCCACCATATT
CCAATACCTTGGCCAAAACAGAGG
TCCAGGGGGCCTCCTGCCACCTTG
AGTATAGTCCAGAACGAGGCAAAG
CTGAAGGCAGA<3'
(SEQ ID NO:4)

— Targeting Vector
- - - Endogenous Locus

* Not drawn to scale

FIGURE 2B

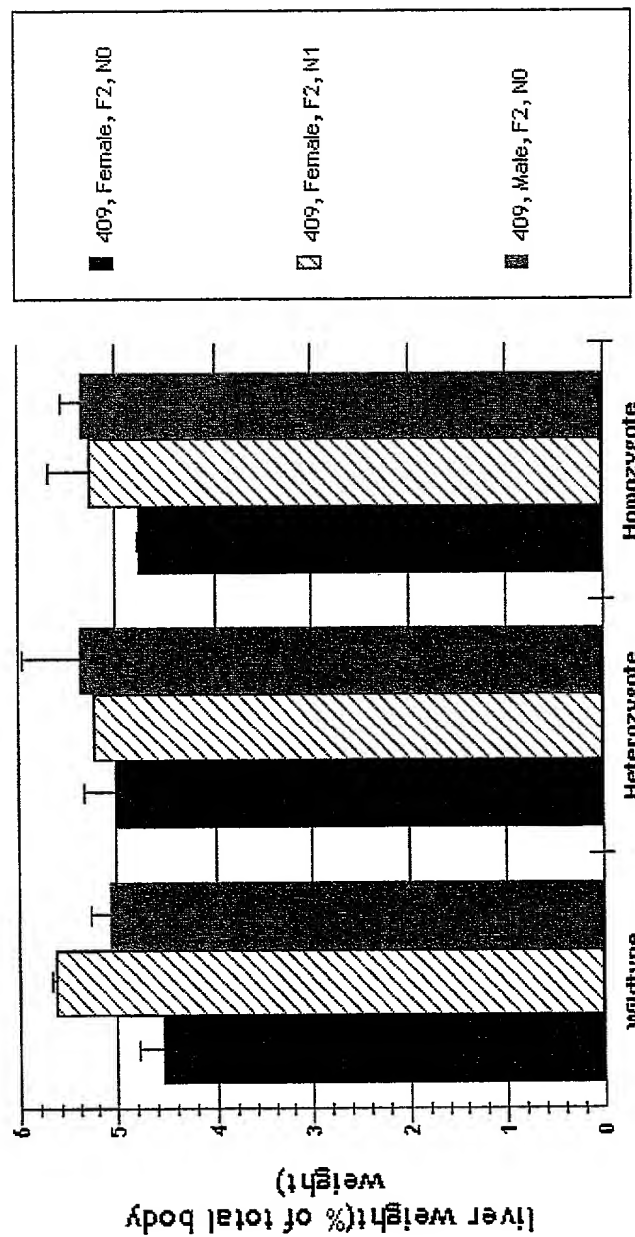
necropsy - spleen weight/body weight



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FIG. 3

necropsy - liver weight/body weight



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FIG. 4

necropsy - kidney weight/body weight

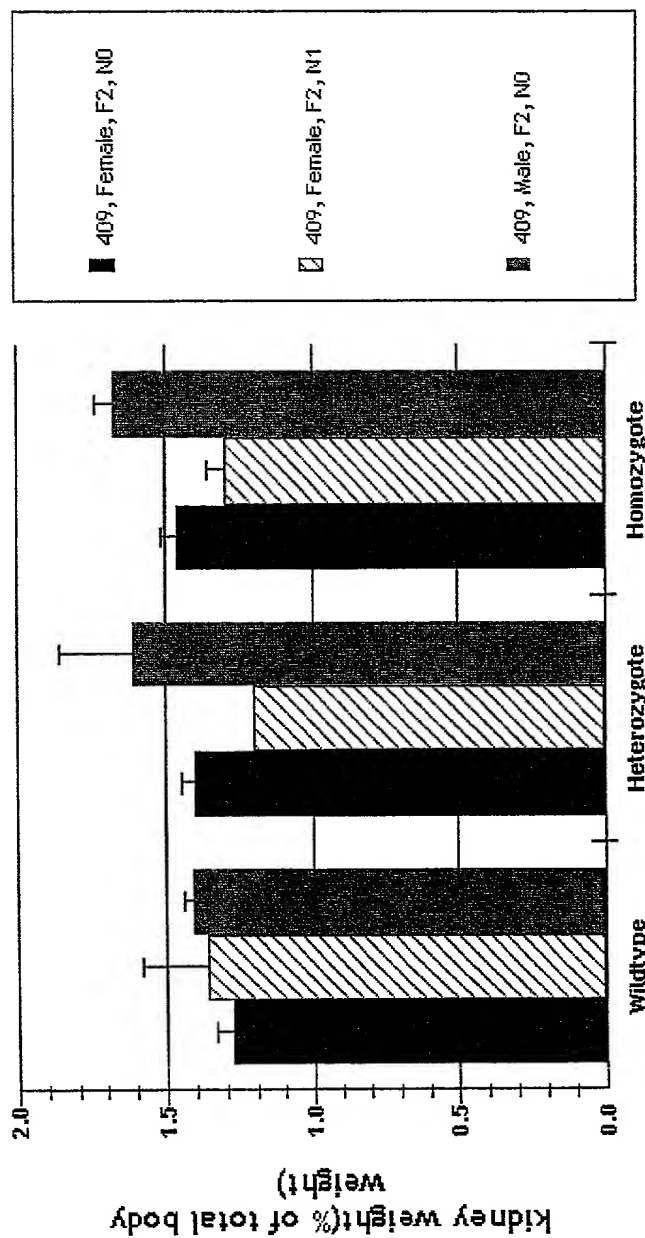


FIG. 5

necropsy - thymus weight/body weight

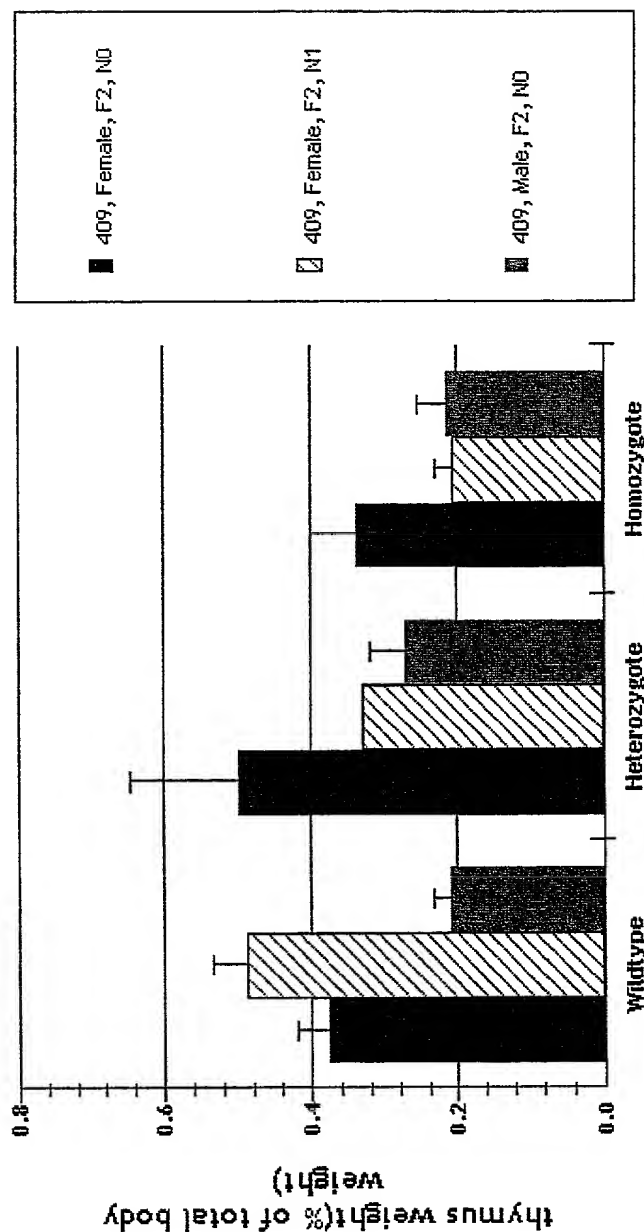


FIG. 6